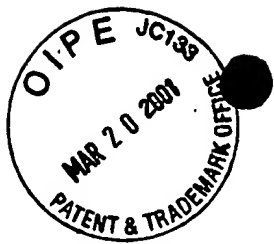


Seq. listing  
4-8



**UNITED STATES DEPARTMENT OF COMMERCE**  
**Patent and Trademark Office**  
Address: COMMISSIONER OF PATENTS AND TRADEMARKS  
Washington, DC 20231

1638	01/11/00	SEULBERGER	H	48141
APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR		ATTORNEY DOCKET NO.

KEIL & WEINKAUF  
1101 CONNECTICUT AVE NW  
WASHINGTON DC 20036

HZ12/0308

RECEIVED

MAR 12 2000

KEIL & WEINKAUF

KRUSE, D	EXAMINER
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1638	
ART UNIT	PAPER NUMBER

03/08/01

7

DATE MAILED:

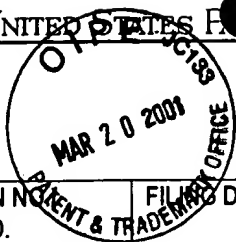
Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



## UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS  
UNITED STATES PATENT AND TRADEMARK OFFICE  
WASHINGTON, DC 20231  
www.uspto.gov



APPLICATION NO. CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
--------------------------------	-------------	---	---------------------

EXAMINER
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ART UNIT	PAPER
----------	-------

7

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

## Commissioner of Patents

The communication filed 5 January 2001 is not fully responsive to the Office communication mailed 18 December 2000 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner David Kruse, Ph.D., Art Unit 1638, whose telephone number is (703) 306-4539.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

David Kruse Art Unit 1638  
7 March, 2001

**AMY J. NELSON, PH.D**  
**PRIMARY EXAMINER**



Application No.

09/462,629

Examiner

David H Kruse

Applicant(s)

SEULBERGER ET AL.

Art Unit

1638

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**



## RAW SEQUENCE LISTING ERROR REPORT

BIOLOGY  
SYSTEMS  
BRANCH

#6  
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FEB 05 2001

TECH CENTER

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/462,629

Source: 1638

Date Processed by STIC: 1/24/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**



# Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/462,629

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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FEB 05 2001

1638



RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/462,629

DATE: 01/24/2001  
 TIME: 13:38:32

Input Set : A:\462629.txt  
 Output Set: N:\CRF3\01242001\I462629.raw

Does Not Comply  
 Corrected Diskette Needed

P3

3 <110> APPLICANT: Seulberger, Harald  
 4 Lerchl, Jenms  
 5 Schmidt, Ralf-Michael  
 6 Krupinska, Karin  
 7 Falk, Jon  
 9 <120> TITLE OF INVENTION: DNA sequence encoding a hydroxyphenylpyruvate  
 dioxygenase, and its  
 10 overproduction in plants  
 11  
 12 <130> FILE REFERENCE:  
 12 <140> CURRENT APPLICATION NUMBER: US 09/462,629  
 13 <141> CURRENT FILING DATE: 2000-01-11  
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/03832  
 16 <151> PRIOR FILING DATE: 1998-06-23  
 18 <160> NUMBER OF SEQ ID NOS: 2  
 20 <170> SOFTWARE: WordPerfect version 6.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1565  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: hppd from barley  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: 9 ... 1313  
 31 <400> SEQUENCE: 1  
 33 cgcacacc atg ccg ccc acc ccc acc acc ccc gcg gct acc ggc gcc gcc50  
 34 Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala  
 35 1 5 10  
 37 gcc gcg gtg acg ccg gag cac gcg cga ccg cac cga atg gtc cgc ttc98  
 38 Ala Ala Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe  
 39 15 20 25 30  
 41 aac ccg cgc agc gac cgc ttc cac acg ctc tcc ttc cac cac gtc gag146  
 42 Asn Pro Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu  
 43 35 40 45  
 45 ttc tgg tgc gcg gac gcc gcc tcc gcc gcc ggc cgc ttc gcg ttc gcg194  
 46 Phe Trp Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala  
 47 50 55 60  
 49 ctc ggc gcg ccg ctc gcc gcc agg tcc gac ctc tcc acg ggg aac tcc242  
 50 Leu Gly Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser  
 51 65 70 75  
 53 gcg cac gcc tcc cag ctg ctc cgc tcg ggc tcc ctc gcc ttc ctc ttc290  
 54 Ala His Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe  
 55 80 85 90  
 57 acc gcg ccc tac gcc aac ggc tgc gac gcc gcc acc gcc tcc ctg ccc338  
 58 Thr Ala Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro  
 59 95 100 105 110  
 61 tcc ttc tcc gcc gac gcc gcg cgc cgg ttc tcc gcc gac cac ggg atc386  
 62 Ser Phe Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile  
 63 115 120 125  
 65 gcg gtg cgc tcc gta gcg ctg cgc gtc gca gac gcc gcc gag gcc ttc434

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/462,629

DATE: 01/24/2001

TIME: 13:38:32

Input Set : A:\462629.txt

Output Set: N:\CRF3\01242001\I462629.raw

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66 Ala Val Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe
67          130          135          140
69 cgc gcc agt cgt cga cgg ggc gcg cgc ccg gcc ttc gcc ccc gtg gac482
70 Arg Ala Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp
71          145          150          155
73 ctc ggc cgc ggc ttc gcg ttc gcg gag gtc gag ctc tac ggc gac gtc530
74 Leu Gly Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val
75          160          165          170
77 gtg ctc cgc ttc gtc agc cac ccg gac ggc acg gac gtg ccc ttc ttg578
78 Val Leu Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu
79 175          180          185          190
81 ccg ggg ttc gag ggc gta acc aac ccg gac gcc gtg gac tac ggc ctg626
82 Pro Gly Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu
83          195          200          205
85 acg cgg ttc gac cac gtc gtc ggc aac gtc ccg gag ctt gcc ccc gcc674
86 Thr Arg Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala
87          210          215          220
89 gca gcc tac atc gcc ggg ttc acg ggg ttc cac gag ttc gcc gag ttc722
90 Ala Ala Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe
91          225          230          235
93 acg gcg gag gac gtg ggc acg acc gag agc ggg ctc aac tcg gtg gtg770
94 Thr Ala Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val
95          240          245          250
97 ctc gcc aac aac tcg gag ggc gtg ctg ctg ccg ctc aac gag ccg gtg818
98 Leu Ala Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val
99 255          260          265          270
101 cac ggc acc aag cgc cgg agc cag ata cag acg ttc ctg gaa cac cac866
102 His Gly Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His
103          275          280          285
105 ggc ggc ccg ggc gtg cag cac atc gcg gtg gcc agc agt gac gtg ctc914
106 Gly Gly Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu
107          290          295          300
109 agg acg ctc agg aag atg cgt gcg cgc tcc gcc atg ggc ggc ttc gac962
110 Arg Thr Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp
111          305          310          315
113 ttc ctg cca ccc ccg ctg ccg aag tac tac gaa ggc gtg cga cgc ctt1010
114 Phe Leu Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu
115          320          325          330
117 gcc ggg gat gtc ctc tcg gag gcg cag atc aag gaa tgc cag gag ctg1058
118 Ala Gly Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu
119 335          340          345          350
121 ggt gtg ctc gtc gat agg gac gac caa ggg gtg ttg ctc caa atc ttc1106
122 Gly Val Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe
123          355          360          365
125 acc aag cca gta ggg gac agg ccg acc ttg ttc ctg gag atg atc cag1154
126 Thr Lys Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln
127          370          375          380
129 agg atc ggg tgc atg gag aag gac gag aga ggg gaa gag tac cag aag1202
130 Arg Ile Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/462,629

DATE: 01/24/2001

TIME: 13:38:32

Input Set : A:\462629.txt

Output Set: N:\CRF3\01242001\I462629.raw

```

131          385          390          395
133 ggt ggc tgc ggc ggg ttc ggc aaa ggc aac ttc tcc gag ctg ttc aag1250
134 Gly Gly Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys
135      400          405          410
137 tcc att gaa gat tac gag aag tcc ctt gaa gcc aag caa tct gct gca1298
138 Ser Ile Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala
139 415          420          425          430
141 gtt cag gga tca taggatagaa gctgggtcctt gta1catggt ctcatggagc 1350
142 Val Gln Gly Ser
144 aaaagaaaaac aatgttgttt gtaatatgcg tcgcacaatt atatcaatgt tataattggt1410
146 gaagctgaag acagatgtat cctatgtatg atgggtgtaa tggatggtag aggggctcac1470
148 acatgaagaa aatgtagcgt tgacattgtt gtacaatctt gcttgcaagt aaaataaaga1530
150 acagattttg agttctgcaa aaaaaaaaaa aaaaa          1565
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 434
155 <212> TYPE: PRT
W--> 157 <213> ORGANISM:
157 <400> SEQUENCE: 2
159 Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala Ala Ala
160 1 5 10 15
162 Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe Asn Pro
163 20 25 30
165 Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu Phe Trp
166 35 40 45
168 Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala Leu Gly
169 50 55 60
171 Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser Ala His
172 65 70 75 80
174 Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe Thr Ala
175 85 90 95
177 Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro Ser Phe
178 100 105 110
180 Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile Ala Val
181 115 120 125
183 Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe Arg Ala
184 130 135 140
186 Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp Leu Gly
187 145 150 155 160
189 Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val Val Leu
190 165 170 175
192 Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu Pro Gly
193 180 185 190
195 Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu Thr Arg
196 195 200 205
198 Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala Ala Ala
199 210 215 220
201 Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe Thr Ala
202 225 230 235 240
204 Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val Leu Ala

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*This numeric identifier AND its response are mandatory. See circled portion of item 12 on Error Summary sheet.*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/462,629

DATE: 01/24/2001

TIME: 13:38:32

Input Set : A:\462629.txt

Output Set: N:\CRF3\01242001\I462629.raw

```

205          245          250          255
207 Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val His Gly
208          260          265          270
210 Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His Gly Gly
211          275          280          285
213 Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu Arg Thr
214          290          295          300
216 Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp Phe Leu
217 305          310          315          320
219 Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu Ala Gly
220          325          330          335
222 Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu Gly Val
223          340          345          350
225 Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe Thr Lys
226          355          360          365
228 Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln Arg Ile
229          370          375          380
231 Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys Gly Gly
232 385          390          395          400
234 Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys Ser Ile
235          405          410          415
237 Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala Val Gln
238          420          425          430
240 Gly Ser

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/462,629

DATE: 01/24/2001

TIME: 13:38:33

Input Set : A:\462629.txt

Output Set: N:\CRF3\01242001\I462629.raw

L:0 M:201 W: Mandatory field data missing. FILE REFERENCE

L:157 M:282 W: Numeric Field Identifier Missing, <213> is required.